

| Result No. | Score | Query Match | Length | DB | ID | Description | |
|------------|-------|-------------|--------|----|----------------------|--------------------|--|
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| 1 | 63.6 | 5.9 | 1141 | 4 | US-09-806-708B-22 | Sequence 22, Appl | |
| 2 | 49.6 | 4.6 | 832 | 4 | US-09-621-976-2813 | Sequence 2813, Ap | |
| 3 | 48.4 | 4.5 | 7218 | 1 | US-08-232-463-14 | Sequence 14, Appl | |
| c | 43.2 | 4.0 | 601 | 4 | US-09-949-016-156050 | Sequence 156050, A | |
| | 42.4 | 3.9 | 54161 | 4 | US-09-949-016-11905 | Sequence 11905, A | |
| 5 | 42 | 3.9 | 78810 | 4 | US-09-949-016-16198 | Sequence 16198, A | |
| 6 | 42 | 3.9 | 78810 | 4 | US-09-949-016-16101 | Sequence 16101, A | |
| 7 | 42 | 3.9 | 237241 | 4 | US-09-621-976-2813 | Sequence 2813, Ap | |
| 8 | 41.6 | 3.9 | 832 | 4 | US-09-621-976-2813 | Sequence 2813, Ap | |
| 9 | 40.8 | 3.8 | 151088 | 4 | US-09-949-016-16240 | Sequence 16240, A | |
| 10 | 40.6 | 3.8 | 487 | 4 | US-09-673-395A-86 | Sequence 86, Appl | |
| 11 | 40.6 | 3.8 | 492 | 4 | US-09-673-395A-110 | Sequence 110, App | |
| 12 | 40.6 | 3.8 | 1497 | 4 | US-09-220-132-94 | Sequence 94, Appl | |
| 13 | 40 | 3.7 | 687 | 3 | US-09-134-001C-1857 | Sequence 1857, Ap | |
| 14 | 40 | 3.7 | 687 | 3 | US-09-134-001C-1857 | Sequence 1857, Ap | |
| 15 | 39.4 | 3.7 | 202111 | 4 | US-09-949-016-13877 | Sequence 13877, A | |
| 16 | 39.4 | 3.7 | 343352 | 4 | US-09-949-016-13498 | Sequence 13498, A | |
| 17 | 39.2 | 3.6 | 522 | 4 | US-09-248-798A-7323 | Sequence 7323, Ap | |
| 18 | 39.2 | 3.6 | 7218 | 1 | US-08-232-463-14 | Sequence 14, Appl | |
| 19 | 39 | 3.6 | 99500 | 3 | US-09-798-096-10 | Sequence 10, Appl | |
| 20 | 38.6 | 3.6 | 1141 | 4 | US-09-806-708B-22 | Sequence 22, Appl | |
| 21 | 38.4 | 3.6 | 3258 | 4 | US-09-328-353-587 | Sequence 587, App | |
| 22 | 38.2 | 3.5 | 246240 | 2 | US-08-724-394A-20 | Sequence 20, Appl | |
| 23 | 38.2 | 3.5 | 246240 | 2 | US-08-724-394A-21 | Sequence 21, Appl | |
| 24 | 38.2 | 3.5 | 246240 | 2 | US-08-724-394A-22 | Sequence 22, Appl | |
| 25 | 38 | 3.5 | 1039 | 4 | US-09-902-540-1280 | Sequence 1280, Ap | |
| 26 | 38 | 3.5 | 87470 | 4 | US-09-949-016-15881 | Sequence 15881, A | |
| 27 | 37.8 | 3.5 | 57178 | 4 | US-09-949-016-13838 | Sequence 12838, A | |

Db 570 TRSGRANNYARABHYGKWNTRWBHSHTWBHBRAGAHHYMBMYBAKCHCKWAKYA 629
Qy 413 GACCAAAATCACCTTCAGCATGTGGT-TTCCTTCATCATCATGATTTCTTTGGTTGAC 471
Db 630 KKYAGAGGSNNNNNNNNNNNNNNATCADDYYAASRWYMANAKWYKYKBAANNAYT 689
Qy 472 AAACATTTCTCGCTCTCAGATGCAAAAAGTCACACTGGGAATGAACCTGTAAAGTGGTGA 531
Db 690 HANNWGCWNNATDTRTMKNNNNNNNAGTKNNNNNNKNAASAKNYAAAVKAAKHW 749
Qy 532 TTAGTTTGTGATTTAAATTAATAAATCACTTTAGTTTCTCTCTCTCTATGTTGCA 591
Db 750 RWANKWAMRGWHAADAAABTDKENNGAYTKYTTNNNNNTYGVVNTAARDGHWANNNN 809
Qy 592 ATGAATGTAAGTATTTGGGATCCAGTGCTTATAAACCTTCTCTCTTTGTGCACAGAA 651
Db 810 NNNNNNGHSDMWVWYAWYNTNNNNNNNNYAWWTKNWTYTTDDRWBRBAYTNN 869
Qy 652 TGTAACCTAGCAAGCCCATTAGCACCCAGATAATCTCATGTATGTAGTTCCCATCTCGGA 711
Db 870 NNRMYAYGAYADDYAYMSDTCDAWKKWDATKNNNATTYNRGTAWRTNNNNNNMTKX 929
Qy 712 AAATCTTTGACAGTGGGAAGTCCCGAGTGTGTTTCTTTCTTAGTGGAAGGTGGC 771
Db 930 YBHAANNNNNGKMCCTAHTWVCKATKTTKGCWNNCTTTCRKYKNNCTWYTWMTTTR 989
Qy 772 TAT-ATCACTTTTGAATTTTGCATCTCTTAGACTTTTAAATATATACTAATGATCTA 830
Db 990 TWYAATRWKNNATGSMTRCNATGKNNNNYWGKTRWATYRMATRMWKAWKVMTGWS 1049
Qy 831 GTCTTACTCTAAAGACCTTTGATGTTAAAGAAATCCCTTCATTATTTTCAATATCCCTATC 890
Db 1050 NTSYARWAYKTRAYKGYYNACAWRWGKATCYMTDNNWTTACATSWATHKYNHMC 1109
Qy 891 TCATAGGCGCACAA 904
Db 1110 KNNNNNNNTMR 1123

RESULT 2
US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match 4.6%; Score 49.6; DB 4; Length 832;
Best Local Similarity 13.9%; Pred. No. 0.0011;
Matches 54; Conservative 181; Mismatches 150; Indels 3; Gaps 2;
Qy 566 GTTTTCTCTCTCTCTATGTCGAATGAATGAAATGATTTGGGATCCAGTCTTATA 625
Db 2 RWTWKYTTTAKCTWKKSWSYWKYKTKYWRKWKKKKAWKWKYTWYWR 61
Qy 626 AACCTTCTCTCTCTGTCACAGAAATGTAACCTAGCAGCCCATTAGCACCCAGATATT 685
Db 62 YAMWGYKKKAMCRKTTKKKKKKGYMMWYWGWRSSYMAWMTRTWTGYAYRSMYWR 121

Qy 686 CTATCATGTTAGTTTCCCATCTCGGAAATCTTTGTACAGTGGGAAGTTCCCGATGTGT 745
Db 122 RCHK--KXAYRKTTCYSGKGTWKKWKKAWTTWKKTYWAAATRYWMMCMWTKEWRA 179
Qy 746 TTTTCTTTCTTAGGTGAAGGTTGGCTATATCATCTTTATTGAATTTTGCATTTCTTAGAC 805
Db 180 SMWYCWNGKARKSTWRKRSYASARSKRCCYSCSWGAMSKYMMWRWRGATGAG 239
Qy 806 TTTTAAATATATAATGATTTCTTAGCTTCTTACTCTAAAGACCTTTGATGTTAAAGGA-AT 864
Db 240 MKAWRASCMRRKYAGKSKTSYKSMWMCWTRSKYCYTKARWTGYCYRKGWGWKRGRW 299
Qy 865 CTTCTATTATTTCATATTCCTCTATCTCATAGGCCACAAATTATTTTAAATACAGAGATGA 924
Db 300 YASKYMKWKKWCHWARMYRSTGTTRASWRRWYTTMMKKWKYAWABAARWAMWMA 359
Qy 925 TTTTCAAAATATTTTAACTCGGTACA 952
Db 360 WRRACAAAATATAATTATTATTATGATACA 387

RESULT 3
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14
Query Match 4.5%; Score 48.4; DB 1; Length 7218;
Best Local Similarity 4.8%; Pred. No. 0.0061;

;/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;/ FILE REFERENCE: CL001307
;/ CURRENT APPLICATION NUMBER: US/09/949,016
;/ CURRENT FILING DATE: 2000-04-14
;/ PRIOR APPLICATION NUMBER: 60/241,755
;/ PRIOR FILING DATE: 2000-10-20
;/ PRIOR APPLICATION NUMBER: 60/237,768
;/ PRIOR FILING DATE: 2000-10-03
;/ PRIOR APPLICATION NUMBER: 60/231,498
;/ PRIOR FILING DATE: 2000-09-08
;/ NUMBER OF SEQ ID NOS: 207012
;/ SOFTWARE: FastSeq for Windows Version 4.0
;/ SEQ ID NO 16198
;/ LENGTH: 78810
;/ TYPE: DNA
;/ ORGANISM: Human
;/ FEATURE:
;/ NAME/KEY: misc_feature
;/ LOCATION: (1)...(78810)
;/ OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16198

Query Match 3.9%; Score 42; DB 4; Length 78810;
Best Local Similarity 67.0%; Pred. No. 1.1;
Matches 75; Conservative 0; Mismatches 35; Indels 2; Gaps 1;

Qy 775 ATCACTTATTGATTTGGTTCCTTAGACTTTTAAATATACTAATGTTATCT--AGT 832
Db 46800 ATCACTGCACTGGAGTTCTCATCTCTTTGACTCTTAAATAGATGAATATTTTCCAT 46859

Qy 833 CTTACTCTAAAGACCTTTGATGTTAAAGGAATCTTCATTTTTCATATTC 884
Db 46860 TTATCTTAAAGACATGTGAAGTGTGATCTTGTCTATCTTTCATATTC 46911

RESULT 7
US-09-949-016-16101/c
;/ Sequence 16101, Application US/09949016
;/ Patent No. 6812339
;/ GENERAL INFORMATION:
;/ APPLICANT: VENTER, J. Craig et al.
;/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;/ FILE REFERENCE: CL001307
;/ CURRENT APPLICATION NUMBER: US/09/949,016
;/ CURRENT FILING DATE: 2000-04-14
;/ PRIOR APPLICATION NUMBER: 60/241,755
;/ PRIOR FILING DATE: 2000-10-20
;/ PRIOR APPLICATION NUMBER: 60/237,768
;/ PRIOR FILING DATE: 2000-10-03
;/ PRIOR APPLICATION NUMBER: 60/231,498
;/ PRIOR FILING DATE: 2000-09-08
;/ NUMBER OF SEQ ID NOS: 207012
;/ SOFTWARE: FastSeq for Windows Version 4.0
;/ SEQ ID NO 16101
;/ LENGTH: 237241
;/ TYPE: DNA
;/ ORGANISM: Human
;/ FEATURE:
;/ NAME/KEY: misc_feature
;/ LOCATION: (1)...(237241)
;/ OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16101

Query Match 3.9%; Score 42; DB 4; Length 237241;
Best Local Similarity 47.4%; Pred. No. 1.8;
Matches 126; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

Qy 678 AGATAATCTCATGCTTAGTTTCCCATCTCGGAATCTTTGTACAGTGGAGTTCCC 737
Db 194379 AGCTAATTAGACTATTATTATTCATTAATAAACCTCAGAAACATGAAGTATTTTAC 194320

Qy 738 CGATGTGTTTTCTTCTTAGGTGAAGGGTTGGCTATATCACTTTATTGAATTTTGCATT 797

Db 194319 TGATAATAAAATGTTTTATTATTAGGTAAATGATAACAATGAAACTTAAAGATATAAAACAAT 194260
Qy 798 CCTTAGACTTTTAAATATACTAATGTATTCTTACTTCTTAAAGACCTTTTGATCTTA 857
Db 194259 AGGTATTTTCTTCATATCTGCTCTTAAATCTAGGCTTTTCATGTTAGATCCTCTTTAAA 194200
Qy 858 AAGGAATCCTTTTCATTTTATTTCATATCCCTATCTCATAGGGCCACCAATTTTAAATACA 917
Db 194199 AAGGTATGTAATAATTAATTTTGTAGTTAGTATATAAATATACATATGCTTATAA 194140
Qy 918 GAGATGATTTTCAAAATATTTTAAACA 943
Db 194139 GTAAAAAATATTGAAATATAAATAA 194114

RESULT 8

US-09-621-976-2813/c
;/ Sequence 2813, Application US/09621976
;/ Patent No. 6639063
;/ GENERAL INFORMATION:
;/ APPLICANT: Dumas Milne Edwards, J.B.
;/ APPLICANT: Jobert, S.
;/ APPLICANT: Giordano, J.Y.
;/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;/ FILE REFERENCE: GENSET.054PR2
;/ CURRENT APPLICATION NUMBER: US/09/621,976
;/ CURRENT FILING DATE: 2000-07-21
;/ NUMBER OF SEQ ID NOS: 19335
;/ SOFTWARE: Patent.pm
;/ SEQ ID NO 2813
;/ LENGTH: 832
;/ TYPE: DNA
;/ ORGANISM: Homo sapiens
;/ FEATURE:
;/ NAME/KEY: CDS
;/ LOCATION: 235..399
US-09-621-976-2813

Query Match 3.9%; Score 41.6; DB 4; Length 832;
Best Local Similarity 10.1%; Pred. No. 0.17;
Matches 38; Conservative 173; Mismatches 167; Indels 0; Gaps 0;

Qy 591 AATGAATGTAAGCTATTTTGGGATCCAGTCGTTATAAACCTTTCTCTTCTTTGTGCACAGA 650
Db 378 AATAATATATTTTGTGYYTWTWTKTWYTYTTRMMWKKARRWYWKSYACASRY 319
Qy 651 ATCTAACTAGCAAGCCCATTTAGCACCCAGATAATTTATCATGTTAGTTTCCCATCTCGG 710
Db 318 RKYTWGWWYMKRMWSTRWYCYMKWCKCMYRGRRCAWYTMARGRWMSYAWGKWKMSRSA 259
Qy 711 AAAATCTTTGTACAGTGGGAAGTTCCTCCGATGTGTTTCTTCTTAGGTGAAGGGTTGG 770
Db 258 MSMCTRMYYKGGSTYWTMKTCTATWCYWKYKRWMSKTCWSGSRGGMYSYTSRYS 199
Qy 771 CTATATCACTTTTATGCAATTTTTCATTTCTTAGACTTTTAAATATACTAATGTTATCTA 830
Db 198 MYWASHMYTMCWWGRWSTYTWANGKWRVATTTWRRAMWMAATWMMWYMWAWCM 139
Qy 831 GTCTTACTTAAAGACCTTTTGATGTTTAAAGAAATCCCTTCATTTATTTCATATTCCTTC 890
Db 138 SSRGAAMYRRTMMWGYRWKKSYYRTRCAWAYAKTKRSYVWCWYKWKRCMMWMM 79
Qy 891 TCATAGGGCCACAATTTTAAATACAGAGATGATTTTCAAAATATTTTAACTGTA 950
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Qy 951 CAGACAGATGCCAGCA 968
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RESULT 9

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US-09-949-016-16240/c
; Sequence 16240, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16240
; LENGTH: 151088
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(151088)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16240

Query Match          3.8%; Score 40.8; DB 4; Length 151088;
Best Local Similarity 50.5%; Pred. No. 3.1;
Matches 99; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

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Db      61026 TAGACATCATATCCACTGCTTTAAACTGAATTTCTTTAAATAACATAAATAAAA 60967

Qy      861 GAATCCTTCATTATTTTCATATCCCTATCTCATAGGCCACAAATATTTTAAATACAGAG 920
Db      60966 ATAAACTGCATTTCTTAAATCATTAACAAGTGAGGAGGCCACCTTTTCATACATTCAC 60907

Qy      921 ATGATTTTCAAAATATTTTACAACTGTTACAGACAGATGCCAGCCACTCAGAGGGAT 980
Db      60906 GTCAATTTTAAACACTATTTTCTACTTTTCCAGTTTGTGGCATGTCTTTTAAATGTAT 60847

Qy      981 GCCTGCTGTAACAAG 996
Db      60846 GGTACTTTTGGACAG 60831

RESULT 10
US-09-673-395A-86/c
; Sequence 86, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-673-395A-86

Query Match          3.8%; Score 40.6; DB 4; Length 487;
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Best Local Similarity 73.2%; Pred. No. 0.26;
Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy      931 AAATATTTTAACTGCTACAGCAGACATGCCAGCCACTCAGAAGGATCCCTGCTGTA 990
Db      351 AAATGTTTAACTGCTATAGCATAGACTCCCAACCAATCAGATGGATTTTCAGCCATA 292

Qy      991 AACAAAGCAGTA 1001
Db      291 AACTGCCAGTA 281

RESULT 11
US-09-673-395A-110/c
; Sequence 110, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-673-395A-110

Query Match          3.8%; Score 40.6; DB 4; Length 492;
Best Local Similarity 73.2%; Pred. No. 0.26;
Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy      931 AAATATTTTAACTGCTACAGCAGACATGCCAGCCACTCAGAAGGATCCCTGCTGTA 990
Db      351 AAATGTTTAACTGCTATAGCATAGACTCCCAACCAATCAGATGGATTTTCAGCCATA 292

Qy      991 AACAAAGCAGTA 1001
Db      291 AACTGCCAGTA 281

RESULT 12
US-09-220-132-94/c
; Sequence 94, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: SHYJIAN, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 1497
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1497)
; OTHER INFORMATION: n = A,T,C or G
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 13, 2005, 13:40:12 ; Search time 764 Seconds
(without alignments)
8858.687 Million cell updates/sec

Title: US-09-721-183-1
Perfect score: 1078
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6330947 seqs, 3139163630 residues

Total number of hits satisfying chosen parameters: 12661894

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 1063.8 | 98.7 | 2510 | 17 | US-10-104-047-1599 Sequence 1599, Ap |
| 2 | 1055 | 97.9 | 1879 | 17 | US-10-104-047-1376 Sequence 1376, Ap |
| 3 | 117.6 | 10.9 | 44546 | 13 | US-10-087-192-625 Sequence 625, App |
| C | 4 | 61 | 5.7 | 262 | 11 US-09-864-408A-5207 Sequence 5207, Ap |
| | 5 | 50.4 | 4.7 | 176 | 9 US-09-867-701-9147 Sequence 9147, Ap |
| 6 | 49.4 | 4.6 | 201 | 19 | US-10-741-601-22105 Sequence 22105, A |
| 7 | 49.4 | 4.6 | 201 | 19 | US-10-741-601-22106 Sequence 22106, A |

| | | | | | |
|----|------|------|---------|-------|--|
| 8 | 49.4 | 4.6 | 201 | 19 | US-10-741-601-22107 Sequence 22107, A |
| 9 | 49.4 | 4.6 | 201 | 21 | US-10-741-600-62317 Sequence 62317, A |
| 10 | 49.4 | 4.6 | 201 | 21 | US-10-741-600-62318 Sequence 62318, A |
| 11 | 49.4 | 4.6 | 201 | 21 | US-10-741-600-62319 Sequence 62319, A |
| 12 | 49.4 | 4.6 | 398287 | 19 | US-10-741-601-5719 Sequence 5719, Ap |
| 13 | 49.4 | 4.6 | 398287 | 21 | US-10-741-600-17839 Sequence 17839, A |
| 14 | 49 | 4.5 | 6077 | 15 | US-10-311-455-2192 Sequence 2192, Ap |
| 15 | 48 | 4.5 | 553 | 13 | US-10-027-632-259014 Sequence 259014, A |
| 16 | 48 | 4.5 | 553 | 13 | US-10-027-632-259015 Sequence 259015, A |
| 17 | 48 | 4.5 | 553 | 17 | US-10-027-632-259014 Sequence 259014, A |
| 18 | 48 | 4.5 | 553 | 17 | US-10-027-632-259015 Sequence 259015, A |
| 19 | 46 | 4.3 | 5930 | 15 | US-10-311-455-490 Sequence 490, App |
| 20 | 45.8 | 4.2 | 16811 | 15 | US-10-311-455-1919 Sequence 1919, Ap |
| C | 21 | 45.6 | 4.2 | 16569 | 22 US-10-488-618-1 Sequence 1, Appli |
| | 22 | 44.6 | 4.1 | 5520 | 15 US-10-311-455-1492 Sequence 1492, Ap |
| 23 | 44.2 | 4.1 | 14615 | 18 | US-10-221-714A-430 Sequence 430, App |
| C | 24 | 44 | 4.1 | 7040 | 15 US-10-172-086-13 Sequence 13, Appl |
| | 25 | 44 | 4.1 | 7040 | 18 US-10-221-714A-161 Sequence 161, App |
| C | 26 | 44 | 4.1 | 7040 | 19 US-10-311-507-47 Sequence 47, Appl |
| C | 27 | 44 | 4.1 | 7040 | 20 US-10-480-846-13 Sequence 13, Appl |
| C | 28 | 44 | 4.1 | 7040 | 20 US-10-473-126-173 Sequence 173, App |
| | 29 | 44 | 4.1 | 7040 | 20 US-10-473-126-319 Sequence 319, App |
| 30 | 43.8 | 4.1 | 6076 | 18 | US-10-221-714A-385 Sequence 385, App |
| 31 | 43.8 | 4.1 | 6189 | 15 | US-10-240-485-145 Sequence 145, App |
| 32 | 43.8 | 4.1 | 6189 | 18 | US-10-221-714A-321 Sequence 321, App |
| 33 | 43.6 | 4.0 | 6075 | 15 | US-10-311-455-1523 Sequence 1523, Ap |
| 34 | 43.4 | 4.0 | 15674 | 15 | US-10-311-455-336 Sequence 336, App |
| 35 | 43.4 | 4.0 | 15674 | 15 | US-10-240-485-30 Sequence 30, Appl |
| 36 | 43.2 | 4.0 | 11092 | 15 | US-10-311-455-1485 Sequence 1485, Ap |
| 37 | 43 | 4.0 | 721 | 20 | US-10-363-345A-3373 Sequence 3373, Ap |
| C | 38 | 43 | 4.0 | 721 | 20 US-10-363-345A-3374 Sequence 3374, Ap |
| 39 | 43 | 4.0 | 721 | 21 | US-10-363-483A-3373 Sequence 3373, Ap |
| C | 40 | 43 | 4.0 | 721 | 21 US-10-363-483A-3374 Sequence 3374, Ap |
| C | 41 | 42.8 | 4.0 | 663 | 13 US-10-027-632-236652 Sequence 236652, A |
| C | 42 | 42.8 | 4.0 | 663 | 17 US-10-027-632-236652 Sequence 236652, A |
| 43 | 42.8 | 4.0 | 12138 | 15 | US-10-311-455-1602 Sequence 1602, Ap |
| 44 | 42.8 | 4.0 | 12138 | 17 | US-10-357-166-116 Sequence 116, App |
| 45 | 42.8 | 4.0 | 3673778 | 16 | US-10-312-841-2 Sequence 2, Appli |

ALIGNMENTS

RESULT 1
US-10-104-047-1599
; Sequence 1599, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1599
; LENGTH: 2510
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1599

| | | | | |
|-----------------------|--------------|---|------------|--------------|
| Query Match | 98.7% | Score 1063.8; | DB 17; | Length 2510; |
| Best Local Similarity | 99.7% | Pred. No. 1.9e-259; | | |
| Matches 1076; | Conservative | 0; | Mismatches | 2; |
| | | | Indels | 1; |
| | | | Gaps | 1; |
| Qy | 1 | GGATGATACAGACCCAGGACATTTGAGTTGTCGTTAGATAGGAAAGGATC | 60 | |
| | | | | |
| Db | 1432 | GGATGATACAGACCCAGGACATTTGAGTTGTCGTTAGATAGGAAAGGATC | 1491 | |
| | | | | |
| Qy | 61 | CAGGAAATCAACAGTAAGTGAGATGAGCGGTCTCTTGGTTTTCATTGAGGATAGA | 120 | |
| | | | | |

Qy 840 TAAAGACCTTGTATGTTTAAAGGAATCCTTCAATTTATTTATTTATTTCCCTATCTCATAGGGC 899
Db 1641 TAAAGACCTTGTATGTTTAAAGGAATCCTTCAATTTATTTATTTATTTCCCTATCTCATAGGGC 1700

Qy 900 CACAAATTTTAAATACAGAGATGATTTTCAAAATATTTTAAACAACTGGTACAGGACAGA 959
Db 1701 CACAAATTTTAAATACAGAGATGATTTTCAAAATATTTTAAACAACTGGTACAGGACAGA 1760

Qy 960 TGCAGACCACTCAGAAGGGATCGCTGTGTAACAAGCAGCATATGATGGTTGTACCAATG 1019
Db 1761 TGCAGACCACTCAGAAGGGATCGCTGTGTAACAAGCAGCATATGATGGTTGTACCAATG 1820

Qy 1020 CCTATTGGCTGAACATTTATGCTACTTTTCAGATATTTAAATGGTGTCTTCTTTGAATCGTG 1078
Db 1821 CCTATTGGCTGAACATTTATGCTACTTTTCAGATATTTAAATGGTGTCTTCTTTGAATCGTG 1879

RESULT 3
US-10-087-192-625
; Sequence 625, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087.192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 625
; LENGTH: 44546
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(44546)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-625

Query Match 10.9%; Score 117.6; DB 13; Length 44546;
Best Local Similarity 64.3%; Pred. No. 2.1e-18;
Matches 297; Conservative 0; Mismatches 139; Indels 26; Gaps 7;

Qy 210 TTTCTAGATATCTGGGAAAGATTTGATAATAGTTGTTTGTGAATAGAAAGGAGGATATGA 269
Db 35036 TTTTCTTAAGTCTAGGAAGTCTTGCTACAGCTGTTGTAGGAAGGAGGTGGAT-CGG 35094

Qy 270 TGTGTTTATGCGCATTTTGGCGGACTCTTCGACTTCTGCTGCTCTCTTGAAGTATAC 329
Db 35095 GGCTGCTCGCGTCTCTGTGTGAACCTGTTTGACTTGATGCTGTCTCTGCTGCTGCTG 35154

Qy 330 ATTCCATTCATCTCGCGAGATCCAGTCTTACGTACTGCTCTCTTCTAGCTGCTTAG 389
Db 35155 ATTGTTAAACCCCTGGAGAGCCCGAGTGTCTATGGA--TGTCCTCTTAGCTGCTTAG 35212

Qy 390 -----AGTAAACGATCATCAGTTCAATGGACCAAAATCACCTTCAGCATGTGTTTCT 443
Db 35213 TCGGAGAACCATCATCATCTCACTCGGTGGAGCCCAACCGCATCAGCATGTG---ACT 35269

Qy 444 TCATCATCATGATTTCTTTTGGTTGACAAACATTTCTGGCTCTCAGATGCAAAAAGTCAAC 503
Db 35270 TCCTAATCATGGTTTCTTTTGGTTGACAA--GTTCTGGCTCAGGTG---AAAAGCCAC 35324

Qy 504 ACTGGGAATGACCTGTGAAGTGGTGAATTTAGTTTGGTATTTAATTTAAACACTACATTT 563
Db 35325 ACGAAGAAATGAGCTGTGAAGCGGTGGCATCTTTGGATACCTTAGTTTAAAGTATATGT 35384

Qy 564 TAGTTTTCTTCTCTTCTTCTATGTTGCAATGAATGTAAGTATTTGGATCCAGTGCTTA 623
Db 35385 GTGATTTTCTATGTTCT-----CAAAACTATCATGAGTTTTTGGCCCGAGCAAGTG 35435

Qy 624 TAAACCTTTCTTCTTCTTGTGACAGAAATGTAACACTAGCAAGC 665
Db 35436 TAGACCTCCCTTCTTGTGCCCAGACTGTGACTAGTAGGAC 35477

RESULT 4
US-09-864-408A-5207/c
; Sequence 5207, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Enc
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5207
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-864-408A-5207

Query Match 5.7%; Score 61; DB 11; Length 262;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATGATACAGAGCCCAAGGACACATTTTCAGTTGTGTCGCTTAGATAGGAAAGGATC 60
Db 61 GGATGATACAGAGCCCAAGGACACATTTTCAGTTGTGTCGCTTAGATAGGAAAGGATC 2

Qy 61 C 61
Db 1 C 1

RESULT 5
US-09-867-701-9147
; Sequence 9147, Application US/098677701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9147
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-9147

Query Match 4.7%; Score 50.4; DB 9; Length 176;
Best Local Similarity 78.2%; Pred. No. 0.015;
Matches 86; Conservative 0; Mismatches 21; Indels 3; Gaps 2;

Qy 964 AGCCACTCAGAAGGGATCGCTG--CTGTAAACAAGCAGTATGTATGTTGTACCAATGCC 1021
Db 30 AGAACCACAGAGGGATGGCTTGGTTGGAACACCCGCTATGATTTGGTGGACCATGCC 89

